

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 1, 2006, 10:41:26 ; Search time 142 Seconds

(without alignments)
963.889 Million cell updates/sec

Title: US-10-604-944A-14

Perfect score: 77
Sequence: 1 ttaccctatgtagcagaca.....aaccttaaatgcatggttaa 77

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents NA: *
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2: /cgn2_6/ptodata/1/ina/5 COMB. seq: *
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8: /cgn2_6/ptodata/1/ina/6 COMB. seq: *
9: /cgn2_6/ptodata/1/ina/6 COMB. seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	77	100.0	840	2	US-07-979-966A-1
2	77	100.0	845	2	US-08-589-446-3
3	77	100.0	845	2	US-08-444-882-3
4	77	100.0	845	2	US-08-389-459A-3
5	77	100.0	845	3	US-08-987-867A-3
6	77	100.0	1314	3	US-08-392-794A-1
7	77	100.0	2095	2	US-08-333-901-5
8	77	100.0	2095	2	US-08-456-582-5
9	77	100.0	2095	2	US-08-898-789-5
10	77	100.0	3807	2	US-08-417-210A-78
11	77	100.0	3807	2	US-09-136-159A-78
12	77	100.0	4307	3	US-09-552-950-1
13	77	100.0	4307	3	US-09-936-572-1
14	77	100.0	4338	3	US-09-872-733A-1
15	77	100.0	5362	3	US-08-463-209-5
16	77	100.0	5362	3	US-08-463-209-5
17	77	100.0	5362	3	US-08-463-209-5
18	77	100.0	7228	2	US-08-850-049-128
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20	77	100.0	7228	2	US-08-050-478-128
21	77	100.0	7228	2	US-08-050-478-128
22	77	100.0	7228	2	US-09-414-117-128
23	77	100.0	7228	3	US-09-414-117-128
24	77	100.0	7228	3	US-09-678-437-128

25	77	100.0	7228	3	US-09-678-437-129	Sequence 129, App
26	77	100.0	7228	3	US-09-943-722-128	Sequence 128, App
27	77	100.0	7228	3	US-09-943-722-129	Sequence 129, App
28	77	100.0	8366	3	US-09-872-733A-6	Sequence 6, Appl
29	77	100.0	8560	3	US-09-936-572-11	Sequence 11, Appl
30	77	100.0	8932	3	US-09-124-900-1	Sequence 1, Appl
31	77	100.0	8933	3	US-08-463-210-4	Sequence 4, Appl
32	77	100.0	8933	3	US-09-620-958A-3	Sequence 3, Appl
33	77	100.0	8933	3	US-09-620-958A-4	Sequence 4, Appl
34	77	100.0	8933	3	US-08-463-209-4	Sequence 9, Appl
35	77	100.0	8933	3	US-08-463-209-4	Sequence 9, Appl
36	77	100.0	8933	3	US-09-943-286-3	Sequence 4, Appl
37	77	100.0	8933	3	US-09-943-286-4	Sequence 4, Appl
38	77	100.0	8933	3	US-09-943-286-9	Sequence 9, Appl
39	77	100.0	8933	3	US-09-827-688-4	Sequence 4, Appl
40	77	100.0	9609	3	US-09-700-304-1	Sequence 1, Appl
41	77	100.0	9719	3	US-09-393-795-2	Sequence 2, Appl
42	75.4	97.9	1503	3	US-08-418-848A-9	Sequence 9, Appl
43	75.4	97.9	7399	2	US-08-188-583-5	Sequence 5, Appl
44	75.4	97.9	9709	2	US-08-388-353-1	Sequence 1, Appl
45	75.4	97.9	9709	3		

ALIGNMENTS

RESULT 1
US-07-979-966A-1
; Sequence 1, Application US/07979966A
; Patent No. 5707864
GENERAL INFORMATION:
APPLICANT: Myron E. Essex
APPLICANT: Xiaofang Yu
TITLE OF INVENTION: AIDS THERAPEUTICS BASED ON HIV
NUMBER OF INVENTION: NA PEPTIDES
CORRESPONDENCE ADDRESS:
ADDRESS: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/979,966A
FILING DATE: No. 5707864ember 23, 1992
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: John W. Freeman
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00379/018001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 840
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-07-979-966A-1
Query Match 100.0%; Score 77; DB 2; Length 840;

EDJ

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OM nucleic - nucleic search, using sw model

Run on: February 1, 2006, 10:44:30 ; Search time 816 Seconds
(without alignments)
780.321 Million cell updates/sec

Title: US-10-604-944a-14

Perfect score: 1 ttaccctatgctgcagaaac.....aacttaaatgcatggttaa 77

Sequence: IDENTITY_NUC

Scoring table: Gapop 10.0, Gapext 1.0

Searched: 9793542 seqs, 413468905 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications_NA_Main:*

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7: /cgn2_6/prodata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/prodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/prodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/prodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	77	100.0	845	US-09-756-551A-3	Sequence 3, Appl
3	77	100.0	1092	US-10-003-035-34	Sequence 34, Appl
4	77	100.0	1092	US-10-286-332A-34	Sequence 34, Appl
5	77	100.0	1092	US-10-280-915-34	Sequence 34, Appl
6	77	100.0	1092	US-10-286-332A-34	Sequence 34, Appl
7	77	100.0	1092	US-10-280-915-34	Sequence 34, Appl
8	77	100.0	1179	US-10-003-035-35	Sequence 35, Appl
9	77	100.0	1179	US-10-286-332A-35	Sequence 35, Appl
10	77	100.0	1179	US-10-280-915-35	Sequence 35, Appl
11	77	100.0	1179	US-10-286-332A-35	Sequence 35, Appl
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14	77	100.0	1308	US-10-286-332A-36	Sequence 36, Appl
15	77	100.0	1308	US-10-280-915-36	Sequence 36, Appl
16	77	100.0	1308	US-10-286-332A-36	Sequence 36, Appl
17	77	100.0	1308	US-10-280-915-36	Sequence 36, Appl
18	77	100.0	1496	US-10-003-035-17	Sequence 17, Appl
19	77	100.0	1496	US-10-286-332A-17	Sequence 17, Appl
20	77	100.0	1496	US-10-280-915-17	Sequence 17, Appl
21	77	100.0	1496	US-10-286-332A-17	Sequence 17, Appl
22	77	100.0	1496	US-10-280-915-17	Sequence 17, Appl
23	77	100.0	1503	US-09-968-355-25	Sequence 25, Appl

24	77	100.0	1503	US-10-097-534-31	Sequence 31, Appl
25	77	100.0	1503	US-10-000-511A-9	Sequence 9, Appl
26	77	100.0	1503	US-10-000-511A-10	Sequence 10, Appl
27	77	100.0	1503	US-10-384-339C-138	Sequence 138, Appl
28	77	100.0	1503	US-10-844-658-8	Sequence 8, Appl
29	77	100.0	1515	US-10-102-622-5	Sequence 5, Appl
30	77	100.0	1548	US-09-968-355-19	Sequence 19, Appl
31	77	100.0	1596	US-09-968-355-22	Sequence 22, Appl
32	77	100.0	1621	US-09-882-945A-158	Sequence 158, Appl
33	77	100.0	1621	US-10-807-114-158	Sequence 158, Appl
34	77	100.0	1752	US-09-968-355-16	Sequence 16, Appl
35	77	100.0	1800	US-10-003-035-58	Sequence 58, Appl
36	77	100.0	1800	US-10-286-332A-58	Sequence 58, Appl
37	77	100.0	1800	US-10-280-915-58	Sequence 58, Appl
38	77	100.0	1800	US-10-286-332A-58	Sequence 58, Appl
39	77	100.0	1800	US-10-280-915-58	Sequence 58, Appl
40	77	100.0	2460	US-10-483-654-30	Sequence 30, Appl
41	77	100.0	3477	US-10-336-566-87	Sequence 87, Appl
42	77	100.0	3479	US-10-646-628-5	Sequence 5, Appl
43	77	100.0	3807	US-10-441-788-78	Sequence 78, Appl
44	77	100.0	4307	US-09-999-183-1	Sequence 1, Appl
45	77	100.0	4307	US-10-351-938-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-10-604-944-14
; Sequence 14, Application US/10604944
; Publication No. US20040219515A1
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL HIV REGULATORY GENE;
; FILE REFERENCE: 55008
; CURRENT APPLICATION NUMBER: US/10/604,944
; CURRENT FILING DATE: 2003-08-28
; NUMBER OF SEQ ID NOS: 406
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 77
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus 1
US-10-604-944-14

Query Match 100.0%; Score 77; DB 8; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.7e-18;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 TTACCTTATGTCGAAACATTCAGGGGCAATGTCATCAGGCCATATCCTTGAAC 60
QY 61 TTTAATGTCATGGGTAA 77
DB 61 TTTAATGTCATGGGTAA 77

RESULT 2
US-09-756-551A-3
; Sequence 3, Application US/09756551A
; Patent No. US20020051768A1
; GENERAL INFORMATION:
; APPLICANT: C. Morrow et al.
; TITLE OF INVENTION: ENCAPSIDATED RECOMBINANT VIRAL
; TITLE OF INVENTION: NUCLEIC ACID AND METHODS OF MAKING AND
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 STATE STREET
; CITY: BOSTON

605

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OM nucleic - nucleic search, using sw model

Run on: February 1, 2006, 10:52:42 / Search time 405 Seconds
(without alignments)
157.929 Million cell updates/sec

Title: US-10-604-944A-14

Perfect score: 77
Sequence: 1 ttaccctatgctgagaca.....aacttaaatcgtggttaa 77

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 6059551 seqs, 41533918 residues

Total number of hits satisfying chosen parameters: 12119102

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

Published Applications NA New:
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3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:
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5: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
6: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:
7: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:
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11: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	77	100.0	1515	US-11-029-465-5	Sequence 5, Appli
3	77	100.0	9719	US-11-042-988-10	Sequence 10, Appli
4	75.4	97.9	1503	US-10-519-531-2	Sequence 2, Appli
5	75.4	97.9	16360	US-10-519-531-1	Sequence 1, Appli
6	75.4	97.9	17207	US-10-519-531-8	Sequence 8, Appli
7	45.6	59.2	1521	US-11-129-442-22	Sequence 22, Appli
8	44	57.1	1503	US-10-507-928-3	Sequence 3, Appli
9	44	57.1	1503	US-11-029-465-3	Sequence 7, Appli
10	44	57.1	1518	US-10-507-928-7	Sequence 7, Appli
11	44	57.1	1518	US-11-029-465-7	Sequence 7, Appli
12	42.4	55.1	1092	US-11-014-842A-40	Sequence 40, Appli
13	42.4	55.1	5278	US-11-124-602-2	Sequence 2, Appli
14	42.4	55.1	5304	US-11-124-602-1	Sequence 1, Appli
15	28.2	36.6	1329	US-10-750-185-37952	Sequence 37952, A
16	28.2	36.6	1329	US-10-750-623-37952	Sequence 37952, A
17	26.4	34.3	1691140	US-11-091-018-1	Sequence 1, Appli
18	25.8	33.5	697	US-10-750-185-28849	Sequence 28849, A
19	25.8	33.5	697	US-10-750-623-28849	Sequence 28849, A
20	24.8	32.2	127340	US-11-112-908-36	Sequence 36, Appli
21	24.8	32.2	127340	US-11-112-908-35	Sequence 35, Appli
22	24.4	31.7	1086	US-10-750-185-32559	Sequence 32559, A

C 23	24.4	31.7	1086	US-10-750-623-32559	Sequence 32559, A
C 24	24.2	31.4	28033	US-10-829-826B-42	Sequence 42, Appli
C 25	24.2	31.4	28033	US-10-829-826B-43	Sequence 43, Appli
C 26	23.8	30.9	643	US-11-043-752-1480	Sequence 1480, Ap
C 27	23.8	30.9	1280	US-10-750-185-53636	Sequence 53636, A
C 28	23.8	30.9	1280	US-10-750-623-53636	Sequence 53636, A
C 29	23.8	30.9	387780	US-11-095-561-13259	Sequence 13259, A
C 30	23.6	30.6	480	US-10-219-146-33	Sequence 33, Appli
C 31	23.6	30.6	480	US-11-219-146-35	Sequence 35, Appli
C 32	23.6	30.6	480	US-11-219-146-37	Sequence 37, Appli
C 33	23.6	30.6	480	US-11-219-146-39	Sequence 39, Appli
C 34	23.6	30.6	600	US-11-219-146-41	Sequence 41, Appli
C 35	23.6	30.6	600	US-11-219-146-43	Sequence 43, Appli
C 36	23.6	30.6	600	US-11-219-146-45	Sequence 45, Appli
C 37	23.6	30.6	600	US-11-219-146-47	Sequence 47, Appli
C 38	23.6	30.6	752	US-11-219-146-17	Sequence 17, Appli
C 39	23.6	30.6	752	US-11-219-146-19	Sequence 19, Appli
C 40	23.6	30.6	752	US-11-219-146-21	Sequence 21, Appli
C 41	23.6	30.6	752	US-11-219-146-23	Sequence 23, Appli
C 42	23.6	30.6	1151	US-11-219-146-1	Sequence 1, Appli
C 43	23.6	30.6	1151	US-11-219-146-3	Sequence 3, Appli
C 44	23.6	30.6	1151	US-11-219-146-5	Sequence 5, Appli
C 45	23.6	30.6	1151	US-11-219-146-7	Sequence 7, Appli

ALIGNMENTS

EDJ

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RESULT 1
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: Sequence 5, Application US/10507928
: Publication No. US20050266024A1
: GENERAL INFORMATION:
: APPLICANT: POWDERED LIMITED AND GLAXO GROUP LIMITED
: TITLE OF INVENTION: ADJUVANT
: FILE REFERENCE: N. 88232B GCM
: CURRENT APPLICATION NUMBER: US/10/507,928
: CURRENT FILING DATE: 2004-09-17
: NUMBER OF SEQ ID NOS: 12
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 5
: LENGTH: 1515
: TYPE: DNA
: ORGANISM: Artificial sequence
: FEATURE:
: OTHER INFORMATION: nucleotide sequence of the p17/24trNEF insert in p17/24trNEFI
US-10-507-928-5

Query Match      100.0%; Score 77; DB 7; Length 1515;
Best Local Similarity 100.0%; Pred. No. 4.3e-20;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTACCTATGTCGAGAACATCCAGGGGCAATGATACATCAGGCATATCAGCTAGAAC 60
Db 393 TTACCTATGTCGAGAACATCCAGGGGCAATGATACATCAGGCATATCAGCTAGAAC 452
QY 61 TTTAATGATGGGTAA 77
Db 453 TTTAATGATGGGTAA 469

RESULT 2
US-11-029-465-5
: Sequence 5, Application US/11029465
: Publication No. US20050256070A1
: GENERAL INFORMATION:
: APPLICANT: Braum, Ralph P.
: APPLICANT: Thomsen, Lindy
: APPLICANT: Van-Wely, Catherine
: APPLICANT: Ertl, Peter
: TITLE OF INVENTION: Adjuvant
: FILE REFERENCE: 033267-015
: CURRENT APPLICATION NUMBER: US/11/029,465.

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OM nucleic - nucleic search, using sw model

Run on: February 1, 2006, 10:39:26 ; Search time 2175 Seconds
(without alignments)
2012.389 Million cell updates/sec

Title: US-10-604-944a-14

Perfect score: 77
Sequence: 1 ttaccctatgtagcagacaa.....aactttaatgcatggtgaa 77

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	77	100.0	303	13	HIVM3S1
2	77	100.0	303	13	HIVM4S1
3	77	100.0	303	13	HIVM5S1
4	77	100.0	303	13	HIVM6S1
5	77	100.0	303	13	HIVM9S1
6	77	100.0	303	13	AB154280
7	77	100.0	303	13	AB154285
8	77	100.0	303	13	AB154295
9	77	100.0	426	13	AY103237
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12	77	100.0	426	13	AY103241
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14	77	100.0	426	13	AY103243
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16	77	100.0	502	13	AF116068
17	77	100.0	517	13	AF116050
18	77	100.0	536	13	AB112053

19	77	100.0	566	6	101331	Sequence 1
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21	77	100.0	574	13	AB112051	Human imm
22	77	100.0	574	13	AB112052	Human imm
23	77	100.0	574	13	AB112056	Human imm
24	77	100.0	574	13	AB112059	Human imm
25	77	100.0	692	13	AY360925	Human imm
26	77	100.0	729	6	A06256	HIV-1 iso
27	77	100.0	735	13	AF071303	gag
28	77	100.0	738	13	AF170634	HIV-1 iso
29	77	100.0	840	6	179824	Sequence 1
30	77	100.0	845	6	AR044674	Sequence 1
31	77	100.0	845	6	138635	Sequence 3
32	77	100.0	845	6	140606	Sequence 3
33	77	100.0	876	6	A02736	Artificial
34	77	100.0	1089	13	AY656080	HIV-1 iso
35	77	100.0	1093	13	AY134961	HIV-1 iso
36	77	100.0	1094	13	AY134965	HIV-1 iso
37	77	100.0	1094	13	AY134966	HIV-1 iso
38	77	100.0	1095	13	AY134957	HIV-1 iso
39	77	100.0	1095	13	AY134959	HIV-1 iso
40	77	100.0	1095	13	AY134967	HIV-1 iso
41	77	100.0	1308	6	E01254	DNA encodin
42	77	100.0	1424	6	A02742	Artificial
43	77	100.0	1424	6	A19610	Artificial
44	77	100.0	1455	6	A75892	Sequence 3
45	77	100.0	1464	6	A75896	Sequence 7

ALIGNMENTS

CDJ

RESULT 1
LOCUS HIVM3S1
DEFINITION Human immunodeficiency virus type 1, myristylated gag protein p17
(gag) gene, partial cds.
L21498
ACCESSION L21498.1 GI:424696
VERSION gag gene, myristylated gag protein p17.
KEYWORDS Human immunodeficiency virus 1 (HIV-1)
SOURCE Human immunodeficiency virus 1
ORGANISM
Viruses; Retro-transcribing viruses; Retroviridae;
Orthoretrovirinae; Lentivirus; Primate lentivirus group.
REFERENCE
1 (bases 1 to 303)
Zhu, T., Mo, H., Wang, N., Nam, D.S., Cao, Y., Koup, R.A. and Ho, D.D.
Genotypic and phenotypic characterization of HIV-1 patients with
primary infection
Science 261 (5125), 1179-1181 (1993)
JOURNAL
PUBMED
COMMENT
FEATURES
source
Original
location/Qualifiers
1..303
/organism="Human immunodeficiency virus type 1 RNA."
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/translation="TGPALOTGSEPLRSLEPTVATLTCVQKIDVKTETAELEKEE
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ORIGIN

Query Match 100.0%; Score 77; DB 13; Length 303;
Best Local Similarity 100.0%; Pred. No. 8.2e-16;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TTACCTATGTCAGAAATCCAGGGGCAATGTGATCATGAGCCATATCACTAGAAC 60